

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: April 24, 2002, 05:09:43 ; Search time 299.66 seconds  
(without alignments)  
2814.677 Million cell updates/sec

Title: US-09-525-948A-11

perfect score:

Sequence: 1 at different concentrations

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length:	0
Maximum DB seq length:	200000000

### Post-processing: Minimum Match (2)

Maximum Match 100%

List 109 first 45 summaries

Database : FSI: \*

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l: cm_costfun:*
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2: em\_esthum: ★

3: em\_estin: \*

4: em\_estom:★

5: em\_estpl:★

\*:pq7so\_w0 : 9

7: em\_estro:★

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8: em_estov: *
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9: em_hlc:*
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10: qb_est.l:★
11: qb_est.r:★
```

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11: qb_est.2: *
12: qb_est.3: *
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13: qb\_ltc: \*

13: qb\_gsc: \*

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13: qb_gss: *
14: cm_gss: fun:
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14: em\_gss\_for:  
15: em\_gss\_bum:

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15: em_ss_in:
16: em_ss_in:

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16: em_gss_mv:
17: em_gss_pl0:
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17: cm_qss_pro:
18: cm_qss_pro:
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18: cm\_qss\_rod;  
19: cm\_qss\_rod;15: cm\_qss\_vrt;  
20: cm\_qss\_vrt;

21: em\_qss\_oh

100

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query #	Score	Query		DB	ID	Description
			Match	Length			
1	557	92.8	957	10	AL559050	AL559050	
2	555	92.6	827	10	AL552099	AL552099	
3	555	92.5	761	10	AL131978	AL131978	
4	554	92.3	974	11	EG180101	EG180101	
5	541.2	90.7	978	10	AL577009	AL577009	
6	530	88.3	942	10	AL529836	AL529836	
7	489.6	81.6	845	10	AU125921	AU125921	
8	483	80.5	859	10	AU124446	AU124446	
9	480.5	80.1	767	10	AU142156	AU142156	
10	480.4	80.1	664	11	BE71909	BE71909	
11	467	77.5	936	11	HG68148	HG68148	
12	465	77.5	971	11	BF76920	BF76920	

13	464.6	77.4	772	10	AU137940	AU137940	AU137940
14	458.8	75.1	817	10	AU125680	AU125680	AU125680
15	440.4	71.7	735	10	AU124154	AU124154	AU124154
16	427.4	71.2	939	11	B367141	B367141	B367141
17	414.2	69.0	802	10	AU142163	AU142163	AU142163
18	413.8	69.0	805	10	AU125694	AU125694	AU125694
19	413	68.8	712	10	B0549214	B0549214	B0549214
20	412.8	69.4	934	13	A3225833	A3225833	A3225833
21	410.8	68.5	788	10	AU124519	AU124519	AU124519
22	409	69.2	475	10	B2713248	B2713248	B2713248
23	397	66.2	942	11	B3674542	B3674542	B3674542
24	395.4	66.9	932	11	B3269429	B3269429	B3269429
25	386.8	64.5	491	11	B3838822	B3838822	B3838822
26	385.2	64.3	435	11	B2693030	B2693030	B2693030
27	361.6	60.3	742	10	AU123646	AU123646	AU123646
28	359	59.8	934	10	A1186844	A1186844	A1186844
29	358.2	59.7	416	10	B3674950	B3674950	B3674950
30	354.4	59.1	934	11	B6257904	B6257904	B6257904
31	363	58.4	761	11	B3282718	B3282718	B3282718
32	334.4	55.7	634	10	B36756325	B36756325	B36756325
33	329.8	55.0	454	11	B3674789	B3674789	B3674789
34	311.6	51.9	632	10	AU139183	AU139183	AU139183
35	310.6	51.8	779	10	A1119348	A1119348	A1119348
36	307.4	51.2	652	10	AU137288	AU137288	AU137288
37	302.2	50.4	745	11	B36761025	B36761025	B36761025
38	292	50.2	1045	11	B3714218	B3714218	B3714218
39	309.4	50.1	926	11	B3730370	B3730370	B3730370
40	299.8	50.0	706	11	B3690651	B3690651	B3690651
41	297.4	49.5	578	11	B3724891	B3724891	B3724891
42	296.8	48.3	652	10	AU127116	AU127116	AU127116
43	298.2	48.4	674	11	B1146391	B1146391	B1146391
44	293	48.3	722	11	B1414368	B1414368	B1414368
45	288	48.0	351	11	B3767910	B3767910	B3767910

## A: I'm fine.

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RESULT 1
AL559050
LOCUS       957 bp, mRNA, EST
DEFINITION AL559050.111.NT1006-102 Homo sapiens cDNA (clone CS000404305.5
            prime, mRNA sequence, EST)
ACCESSION   AL559050
VERSION     AL559050.1 GI:12404166
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
            1 (bases 1 to 957)
AUTHORS     Li, W., Gruber, C., Jessee, J., and Polayes, D.
TITLE       Full length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BF 191 51006, EVRY (exex) - France
            Email: seq@genoscope.cns.fr, Web: www.genoscope.cns.fr.
FEATURES
            1..957
            /organism="Homo sapiens"
            /cdate="20010904"
            /clone="AL559050.111"
            /clone_lib="NT1006-102"
            /cseq="single"
            /cseq_method="1" value="from library"
            /note="Vector: pCMVScript, 5' primer: NotI, 3' strand cDNA
            was primed with a NotI-poly(dI) primer, 5' primer: cDNA
            enriched, double stranded cDNA was digested with NotI and
            cloned into the NotI and EcoRV sites of the pCMVSPORT 6
            vector. Library was normalized. Library was constructed by
            the technologies. Contact: Feng Bian, Life Technologies,
            a division of Invitrogen, 9600 Medical Center Drive

```







ED	633	GAAITIAWASA; AIGIAGASA; IYAGA; AGASA; BGA.
RESULT	7	
AUT125021		
Locus	845 bp	mRNA
DEFINITION	AUT125021 NTERM4 Homo sapiens cDNA clone NT-ERM4 (2996 nt), mRNA sequence.	EST 24 OCT-2000
ACCESSION	AUT125021	
VERSION	AUT125021.1	GI:10949747
KEYWORDS	EST.	
SOURCE	Human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo;	
AUTHORS	1. (Bases 1 to 845) Ogawa, Wakamatsu, Kikuchi, M., Ishihara, Saito, K., Yamamoto, J., Rajasekharan, V., Nakamura, T., Katsunuma, Taniguchi, Yamanaka, and Isoda, T.	
TITLE	551 Human cDNA Project (GenBank, WAKAMATSU, Oogawa, Miyoshi, Saito, Taniguchi, Yamanaka, Kikuchi, Nakamura, Taniguchi, Taniguchi, Taniguchi, Y., Sugano, S., Isoda, T.)	
JOURNAL	Unpublished (2000)	
COMMENT	Contact: Takao Isoda	

[illegible]

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QY 268 agctgctccaaatgcgaagaaatggctcaggtgagatctcttcttgcacagtgagc 327
DB 520 AGTGTCTTAAATGCTGAAGGCAAAATGCTTAAAGTGAAGATCTTCTTGCACAGTGGAC 579
QY 328 cgaacacacagtgatgagagagagagagagagagagagagagagagagagagagag 387
DB 580 cgaacacacagtgatgagagagagagagagagagagagagagagagagagagagag 639
QY 388 ttccagtgatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 447
DB 640 ttccagtgatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 699
QY 448 aaacagaacacagtgatgagagagagagagagagagagagagagagagagagagag 507
DB 700 AAACAGNACAGTGTGACATGCTGATGACAGTGTCTTCTTAAAGAGAAAGAGA-TGTC 758
QY 508 tccctgtaaaacagtgatgagagagagagagagagagagagagagagagagagagag 567
DB 759 TNCGTGACTAACTGTAAGAAAGAGCTT-GAATGCAAGAGTGTGCTGACCTACCC---ANAT 814
QY 568 aaatgtaaaagacactaaagact 589
DB 815 AAATGTTAAGGCACTGAGGACT 836

RESULT 8
AUI24446 859 bp mRNA EST 23-OCT-2000
LOCUS AUI24446 NT2RM4 Homo sapiens cDNA clone NT2RM4000018 5', mRNA
DEFINITION AUI24446 sequence.
ACCESSION AUI24446
VERSION AUI24446.1 GI:10949162
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 859)
AUTHORS Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J.,
Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and
Isoqai,T.
TITLE HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S.,
Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
Y., Sugano,S., Isoqai,T.)
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isoqai
Genomics Laboratory
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-448-52-3951
Fax: 81-448-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..859
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NT2RM4000018"
/cell_line="NT2RM4"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/Note="vector: pME18SFL3; mRNA from uninduced NT2 neuronal
precursor cells"
BASE COUNT 197 a 217 c 220 g 192 t 3 others
ORIGIN
Query Match 80.5%; Score 483; DB 10; Length 859;
Best Local Similarity 92.9%; Prod. No. 5,26-128;
Matches 540; Conservative 0; Mismatches 8; Indels 34; Gaps 2;

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QY 1 atgggacctccacagtgctgacactgctgctgacactgctgctgacactgctgctgac 60
DB 279 ATGGGTCTTAAAGTGAAGGCAAAATGCTTAAAGTGAAGATCTTCTTGCACAGTGGAC 338
QY 61 ggaatataccctccaggggtattg-----ga 87
DB 339 GGAATATACCCCTCAGGGGTATTTCGACTGGTCCCTCACCCTTAGGGGACACGACAAAGAGA 398
QY 88 qatagtgatgctcccaaaagaaatataatccacccctcaaaataaattcgaatttgcgtlacc 147
DB 399 CATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 458
QY 148 aagtgcacacaaaggaactactgtacaataactgtccagcccgaggcagagatacagag 207
DB 459 AAGTGGCTCAAAAGGAACCTATTGTGTACAAATGA-TGTGTAAGCCGAGGAGATAGGAGC 518
QY 208 tgcagtgagtgagagagagagagagagagagagagagagagagagagagagagagag 267
DB 519 TGCAGGCACTGTGACAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 578
QY 268 aatagctccaaatgcgaagaaatggctcaggtgagatctcttcttgcacagtgagc 327
DB 579 AACTGTCTTAAATGCTGAAGGCAAAATGCTTAAAGTGAAGATCTTCTTGCACAGTGGAC 638
QY 328 caggacacagtgctgagtgagagagagagagagagagagagagagagagagagagag 387
DB 639 CAGGCACTGTGACAGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 698
QY 388 ttcagtgcttcaattgcagagctctgcctcaatgcagagagagagagagagagagagag 447
DB 699 TTTCCAGTGTCTTAAATGCTGAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 757
QY 448 aaacagaacacagtgatgagagagagagagagagagagagagagagagagagagag 507
DB 758 AAACAGNACAGTGTGACATGCTGATGACAGTGTCTTCTTAAAGAGAAAGAGA-TGTC 817
QY 508 tccctgtaaaacagtgatgagagagagagagagagagagagagagagagagagagag 549
DB 818 TNCGTGACTAACTGTAAGAAAGAGCTT-GAATGCAAGAGTGTGCTGACCTACCC---ANAT 859

RESULT 9
AUI242156 767 bp mRNA EST 25-OCT-2000
LOCUS AUI242156 THYR01 Homo sapiens cDNA clone THYR0100186 3 5', mRNA
DEFINITION AUI242156 sequence.
ACCESSION AUI242156
VERSION AUI242156.1 GI:11903677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 (bases 1 to 767)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isoqai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isoqai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-448-52-3951
Fax: 81-448-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
source
1..767

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Db 343 AASTGGCAAAAGCAACTTAATTCTAAATATCTCTCAAGGCGGCGGAGATACGGAG 392
QY 208 TATAGGAGTGTGGAGGCACTCTCTCAAGGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAG 267
Db 393 TCGAGGAGTGTGGAGGCACTCTCTCAAGGCTTCAGGAGGAGGAGGAGGAGGAGGAGGAG 452
QY 268 AACTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 327
Db 453 AGCTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 512
QY 328 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
Db 513 CGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
QY 388 TCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
Db 573 TCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
QY 448 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
Db 632 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
QY 507 CTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 565
Db 692 CTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 748
QY 566 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 584
Db 749 AAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 767

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RESULT 13
AUI37990 772 bp mRNA EST 25 OCT 2000
LOCUS AUI37990 PLACE1 Homo sapiens cDNA clone PLACE1007638 5', mRNA
DEFINITION sequence.
ACCESSION AUI37990
VERSION AUI37990 1 -GI-18649511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 772)
AUTHORS Ota,T., Nishikawa,I., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE BRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292 0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
BRI human cDNA project, 5' & 3' end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Source 1..772
/organism "Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1007638"
/clone_lib="PLACE1"
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/note "Vector: pCMV18SP1"
BASE COUNT 184 a 211 c 210 g 163 t 4 others
ORIGIN

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Query Match

77.4%; Score 464.6; DB 10; Length 772;

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Best Local Similarity: 92.5%; E-Val: 1.7e-124;
Matches: 521; Conservative: 0; Mismatches: 5; Indels: 14; Gaps: 2;
QY 7 ATATGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
Db 191 ATATGCTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 250
QY 61 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 87
Db 251 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 310
QY 88 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 147
Db 311 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 376
QY 148 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 207
Db 371 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 436
QY 208 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 267
Db 431 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 490
QY 268 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 327
Db 491 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 550
QY 328 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 387
Db 551 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 610
QY 388 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 447
Db 611 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 670
QY 448 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 506
Db 671 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 730
QY 507 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 529
Db 731 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 753
RESULT 14
AUI25680 817 bp mRNA EST 24 OCT 2000
LOCUS AUI25680 NT28M4 Homo sapiens cDNA clone NT28M402405 5', mRNA
DEFINITION sequence.
ACCESSION AUI25680
VERSION AUI25680 1 -GI-18649511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 817)
AUTHORS Ota,T., Nishikawa,I., Suzuki,Y., Ishii,S., Saito,K., Yamamoto,J.,
Yamamoto,J., Wakamatsu,A., Ota,T., Nishikawa,I., Nakamura,Y., Sugano,S. and
Isogai,T.
TITLE BRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292 0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
BRI human cDNA project, 5' & 3' end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

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